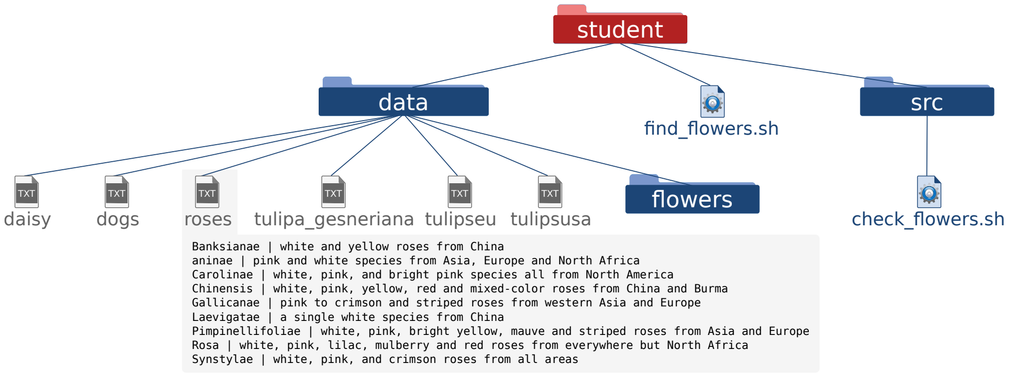
Practical Linux

Practical 2

Core 2

General questions

Let us asume the directory structure presented in Figure 1 with **student** as your **working directory**.



```
Banksianae | white and yellow roses from China
aninae | pink and white species from Asia, Europe and North Africa
Carolinae | white, pink, and bright pink species all from North America
Chinensis | white, pink, yellow, red and mixed-color roses from China and Burma
Gallicanae | pink to crimson and striped roses from western Asia and Europe
Laevigatae | a single white species from China
Pimpinellifoliae | white, pink, bright yellow, mauve and striped roses from Asia and Europe
Rosa | white, pink, lilac, mulberry and red roses from everywhere but North Africa
Synstylae | white, pink, and crimson roses from all areas
```

Figure 1: Directory graph for the general questions section.

1. What command could you use to create a directory named **animals** inside the **data** directory?
   - (a) dir humans
   - (b) mkdir humans
   - (c) crdir data/humans
   - (d) create humans
   - (e) mkdir data/humans
   - (f) this is impossible

2. Assuming that **find_flowers.sh** is an executable script, how would you run it?
   - (a) find_flowers.sh
   - (b) run find_flowers.sh
   - (c) /find_flowers.sh
   - (d) execute /find_flowers.sh
   - (e) ./find_flowers.sh
   - (f) this is impossible

3. What command could you use to move the **find_flowers.sh** file into the **src** directory?
   - (a) mv /find_flowers.sh /src
   - (b) rm find_flowers.sh src
   - (c) move find_flowers.sh src
   - (d) mv find_flowers.sh src
   - (e) cp find_flowers.sh /src
   - (f) this is impossible

4. Assuming that **check_flowers.sh** is an executable script, how would you run it?
   - (a) /src/check_flowers.sh
   - (b) run check_flowers.sh
   - (c) ./check_flowers.sh
   - (d) src/check_flowers.sh
   - (e) execute src/check_flowers.sh
   - (f) this is impossible

5. What command will display the lines containing **red** from the **roses** file?
   - (a) show red roses
   - (b) locate red roses
   - (c) grep red roses
   - (d) find red data roses
   - (e) grep red data/roses
   - (f) this is impossible

6. What command will move only the **tulipseu** and **tulipsusa** files into the **flowers** directory?

(a) mv data/flowers tulips

(b) put into data/flowers data/tulips*

(c) mv data/tulip* data/flowers

(d) move data/flowers data/tulips*

(e) mv data/tulips* data/flowers

(f) this is impossible

Creating and working with directories and files

Make sure that your **working** directory is your **home** directory. (`pwd, cd`)
Run a sequence of commands to make your **home** directory tree look as in Figure 2. This will include:

1. Rename the **project_x** directory to **project_genetics**. (`mv`)
2. Create three **new directories** inside the **project_genetics** directory named: **data**, **src**, **doc**. (`mkdir`)
3. Move the **script.sh** file inside the **project_genetics/src** directory. (`mv`)
4. Move all the **.gb** files from **project_genetics** inside the **project_genetics/data** directory. (`mv, *`)
5. Make a copy of the **project_genetics/README.md** inside **project_genetics/doc**. (`cp`)

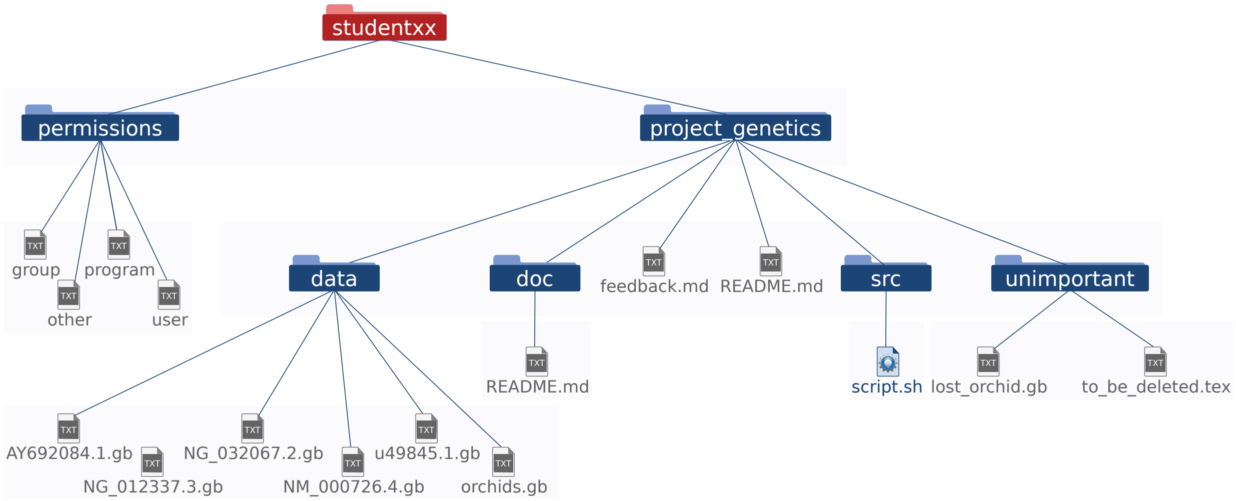


Figure 2: Home directory tree

Remove the **project_genetics/unimportant** directory. (`rm`)

Inspect, edit, and search

1. Print the **project_genetics/README.md** file contents. (`cat`)
2. Open the **project_genetics/README.md** file with `nano` and edit it according to what it is mentioned inside it. (make use of key combinations in `nano`, e.g., `Ctrl-k, Ctrl-x, ...`; see cheat sheet)
3. Print again the **project_genetics/README.md** file content to check the changes. (`cat`)
4. Inspect the **project_genetics/data/orchids.gb** file content first with the `cat` command and after that with the `less` command in order to see the differences between the two commands.
5. Search for the appearences of **LOCUS** within the **project_genetics/data/orchids.gb**. (`grep`)
6. Search for the appearences of **ORGANISM** within all the **.gb** files in the **project_genetics/data** directory. (`grep, *`)

7. Open the **manual** page of **grep** and search for the **option** on how to **suppress the prefixing of file names on output**. (`man`; use the `/` key to search for keywords inside the manual page)
8. Make use of the previous **grep** command found **option** in the search for the appearences of **ORGANISM** within the all **.gb** files in **project_genetics/data**.
9. Rerun the previous command and redirect its output to a file named **organisms.txt** inside the **project_genetics/data** directory. (`grep, *, >`)
10. Check the content of the newly **organisms.txt** created file. (`cat` or `less`)
11. Make sure that your current directory is **project_genetics/data** and run the **project_genetics/src/script.sh** script. A new file **lost_orchid.gb** should appear now in the **project_genetics/data** directory.
12. Append the contents of **lost_orchid.gb** to the **orchids.gb** file. (`cat, >>`)
13. Remove the **lost_orchid.gb** file. (`rm`)
14. Print the first three organisms from the **organisms.txt**. (`head`)
15. What is the total number of organisms that appear in the **organisms.txt** file? (`wc`)
16. What is the disk usage of the data folder? (`du`)

Congratulations, you have finished this practical session!